

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lal, Preeti
Guegler, Karl J.
Corley, Neil C.

(ii) TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
- (B) STREET: 3174 PORTER DRIVE
- (C) CITY: PALO ALTO
- (D) STATE: CALIFORNIA
- (E) COUNTRY: USA
- (F) ZIP: 94304

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: To Be Assigned
- (B) FILING DATE: Herewith
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: CERRONE, MICHAEL C.
- (B) REGISTRATION NUMBER: 39,132
- (C) REFERENCE/DOCKET NUMBER: PF-0527 US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (650) 855-0555
- (B) TELEFAX: (650) 845-4166

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT10
- (B) CLONE: 1691243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met	Val	His	Val	Ala	Tyr	Ser	Leu	Cys	Leu	Pro	Met	Arg	Arg	Ser
														15
5														
Glu	Arg	Tyr	Leu	Phe	Leu	Asn	Met	Ala	Tyr	Gln	Gln	Val	His	Ala
														30
20														
Asn	Ile	Glu	Asn	Ser	Trp	Asn	Glu	Glu	Glu	Val	Trp	Arg	Ile	Glu
														45
35														
Met	Tyr	Ile	Ser	Phe	Gly	Ile	Met	Ser	Leu	Gly	Leu	Leu	Ser	Leu
														60
50														
Leu	Ala	Val	Thr	Ser	Ile	Pro	Ser	Val	Ser	Asn	Ala	Leu	Asn	Trp
														75
65														
Arg	Glu	Phe	Ser	Phe	Ile	Gln	Ser	Thr	Leu	Gly	Tyr	Val	Ala	Leu
														90
80														
Leu	Ile	Ser	Thr	Phe	His	Val	Leu	Ile	Tyr	Gly	Trp	Lys	Arg	Ala
														105
95														
Phe	Glu	Glu	Glu	Tyr	Tyr	Arg	Phe	Tyr	Thr	Pro	Pro	Asn	Phe	Val
														120
110														
Leu	Ala	Leu	Val	Leu	Pro	Ser	Ile	Val	Ile	Leu	Asp	Leu	Leu	Gln
														135
125														
Leu	Cys	Arg	Tyr	Pro	Asp									
140														

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT03
- (B) CLONE: 1999442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Met	Phe	Leu	Pro	Pro	Val	Val	Leu	Ala	Ile	Arg	Ser	Arg	Tyr	Val
														15
5														
Leu	Glu	Ala	Ala	Val	Tyr	Thr	Phe	Thr	Met	Phe	Phe	Ser	Thr	Phe
														30
20														
Tyr	His	Ala	Cys	Asp	Gln	Pro	Gly	Ile	Val	Val	Phe	Cys	Ile	Met
														45
35														
Asp	Tyr	Asp	Val	Leu	Gln	Phe	Cys	Asp	Phe	Leu	Gly	Ser	Leu	Met
														60
50														
Ser	Val	Trp	Val	Thr	Val	Ile	Ala	Met	Ala	Arg	Leu	Gln	Pro	Val
														75
65														
Val	Lys	Gln	Val	Leu	Tyr	Leu	Leu	Gly	Ala	Met	Leu	Leu	Ser	Met
														90
80														
Ala	Leu	Gln	Leu	Asp	Arg	His	Gly	Leu	Trp	Asn	Leu	Leu	Gly	Pro
														105
95														
Ser	Leu	Phe	Ala	Leu	Gly	Ile	Leu	Ala	Thr	Ala	Trp	Thr	Val	Arg
														120
110														
Ser	Val	Arg	Arg	Arg	His	Cys	Tyr	Pro	Pro	Thr	Trp	Arg	Arg	Trp
														135
125														
Leu	Phe	Tyr	Leu	Cys	Pro	Gly	Ser	Leu	Ile	Ala	Gly	Ser	Ala	Val
														150
140														
Leu	Leu	Tyr	Ala	Phe	Val	Glu	Thr	Arg	Asn	Tyr	Phe	Tyr	Ile	

155		160		165
His Ser Ile Trp	His Met Leu Ile Ala	Gly Ser Val Gly Phe	Leu	
170		175		180
Leu Pro Pro Arg	Ala Lys Thr Asp His	Gly Val Pro Ser Gly	Ala	
185		190		195
Arg Ala Arg Gly	Cys Gly Tyr Gln Leu	Cys Ile Asn Glu Gln	Glu	
200		205		210
Glu Pro Gly Pro	Arg Gly Pro Arg Arg	Gly His Cys Gln Gln	His	
215		220		225
Leu Cys Gln Leu	Arg Gly Ala Leu Gly	Leu Ala Leu Arg Gly	Tyr	
230		235		240
Glu Cys Phe Leu	Glu Phe Phe Leu Gly	Val Trp Ser Pro Leu	Arg	
245		250		255
Arg Arg Gln Ala	Val Phe Leu Glu Asp	Met Glu Ser Phe Ser	Arg	
260		265		270
Thr Gln Asn Ser	Ser Arg Asp Leu Glu	Pro Phe Pro Gly	His Gly	
275		280		285
Glu Leu Pro Glu	Gly Leu Glu Ser Pro	Cys Ile Met Glu Ser	Phe	
290		295		300
Leu Arg Thr Gly	Ala Tyr Ala Gly Thr	Glu Ser Leu Arg Thr	Lys	
305		310		315
Glu Ser Leu Leu	Gln Val Trp Ser Leu	Ser Trp Asp Ala Glu	Pro	
320		325		330
Ser Gln Asp Met	Asp Ser Phe Pro Gly	Arg Gln Ser Pro Val	Arg	
335		340		345
Ser Thr Ala Ser	Phe Gln Arg Arg Trp	Ser Leu Ser Trp Gly	Asn	
350		355		360
Gln Ile Ser Arg	Phe Ser Gln Arg Leu	Ser Asn Ser Gly	Leu Arg	
365		370		375
Leu Pro Ser Gln	Arg Gln Arg Leu Gly	Cys Ala Val Leu Trp	Arg	
380		385		390
Arg Asp Cys Arg	Met Asp Gly Ala Gly	Thr Gly Ala Val Trp	Val	
395		400		405
Ala Gly Ile Leu Val				
410				

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: PROSTUT10
 - (B) CLONE: 1691243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

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CAAGTATAGG AGATTTCAC CTTGGTTGGA AACCTGGTTA CAGTGTAGAA AACAGCTTGG 60
ATTACTAAGT TTTTTCTTCG CTATGGCCA TGGTGCTAC AGCCTCTGCT TACCGATGAG 120
AAGGTCAAGAG AGATATTTGT TTCTCAACAT GGCTTATCAG CAGGTCATG CAAATATTGA 180
AAACTCTTGG AATGAGGAAG AAGTTGGAG AATTGAAATG TATATCTCCT TTGGCATAAT 240
GAGCCTTGGC TTACTTTCCC TCCTGGCAGT CACTTCTATC CCTTCAGTGA GCAATGCTTT 300
AAACTGGAGA GAATTCAGTT TTATTCAGTC TACACTTGGA TATGTCGCTC TGCTCATAAG 360
TACTTTCCAT GTTTAATTT ATGGATGGAA ACCAGCTTT GAGGAAGAGT ACTACAGATT 420
TTATACACCA CCAAACTTG TTCTTGCTCT TGTGTTGCC TCAATTGTAA TTCTGGATCT 480

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TTTGCAGCTT	TGCA GATACC	CAGACTGAGC	TGGA ACTGGA	ATTTGTCTTC	CTATTGACTC	540
TACTTCTTTA	AAAGCGGCTG	CCCATTACAT	TCCTCAGCTG	TCCTTGCA GT	TAGGTGTACA	600
TGTGACTGAG	TGTTGGCCAG	TGAGATGAAG	TCTCCTCAA	GGAAGGCAGC	ATGTGTCTT	660
TTTCATCCCT	TCATCTGCT	GCTGGGATTG	TGGATATAAC	AGGAGCCCTG	GCAGCTGTCT	720
CCAGAGGATC	AAAGCCACAC	CCAAAGAGTA	AGGCAGATA	GAGACCAGAA	AGACCTTGAC	780
TACTTCCCTA	CTTCCACTGC	TTTTCTCTGC	ATTAAGCCA	TTGTAATCT	GGGTGTGTTA	840
CATGAAGTGA	AAATTAATTG	TTTCTGCCCT	TCAGTTCTT	ATCCTGATAC	CATTTAACAC	900
TGTCTGAATT	AACTAGACTG	CAATAATTCT	TTCTTTGAA	AGCTTTAAA	GGATAATGTG	960
CAATTACACAT	AAAAATTGAT	TTTCCATTGT	CAATTAGTTA	TACTCATT	CCTGCCTTGA	1020
TCTTTCATTA	GATATTTGT	ATCTGCTTGG	AATATATTAT	CTTCTTTTA	ACTGTGTAAT	1080
TGGAATTAC	AAAAACTCTG	TAATCTCAA	AATATTGCTA	TCAAATTACA	CACCATGTT	1140
TCTATCATTC	TCATAGATCT	GCCTTATAAA	CATTAAATA	AAAAGTACTA	TTAATGATT	1200
AAAAAAAAAA	AAA					1213

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: BRSTTUT03
 - (B) CLONE: 1999442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

CGGACGCGTG	GGCTGCTCTG	CCTGAGCAAC	CTCATGTTTC	TGCCACCTGT	GGTCCTGGCC	60
ATTCGGAGTC	GATATGTGCT	GGAAAGCTGCA	GTCTACACCT	TCACCATGTT	CTTCTCCACG	120
TTCTATCATG	CCTGTGACCA	GCCAGGCATC	GTGGTTTCT	GCATCATGGA	CTACGATGTG	180
CTGCA GTTCT	GTGATTTCCT	GGGCTCTTA	ATGTCCGTGT	GGGTCACTGT	CATTGCCATG	240
GCTCGTTAC	AGCCCGTGGT	CAAGCAGGTG	CTGTATTGTC	TGGGAGCTAT	GCTGCTGTCC	300
ATGGCTCTGC	AGCTTGACCG	ACATGGACTC	TGGAACCTGC	TTGGACCCAG	TCTCTTCGCC	360
CTGGGGATCT	TGGCACACG	CTGGACAGTA	CGCAGCGTCC	GCCGCCGGCA	CTGCTACCCA	420
CCCACGTGGC	GCCGCTGGCT	TTTCTACTTG	TGCCCTGGCA	GCCTTATTGTC	AGGCAGTGCC	480
GTCCTGCTT	ATGTTTTG	GGAGACCCGG	GACA ACTACT	TCTACATTCA	CAGCATTGG	540
CATATGCTCA	TTGCGGGCAG	TGTGGCTTC	CTGCTGCC	CTCGTGC	GA	600
GGGGTCCCCT	CTGGAGCCCG	GGCCCCGGGC	TGTGGTTACC	AGCTATGCAT	CAACGAGCAG	660
GAGGAGCCTG	GGCCTCGTGG	GCCCAGGAGG	GGCCACTGTC	AGCAGCATCT	GTGCCAGCTG	720
AGAGGGGCTT	TGGGCTGGC	CCTGAGGGGA	TATGAATGCT	TCCTAGAGTT	CTTTCTGGG	780
GTGTGGAGCC	CTCTTAGAAG	GAGACAGGCT	GTATTTCTTG	AGGACATGGA	GTCTTCTCA	840
AGGACACAAA	ACTCTTCCAG	GGACCTGGAG	CCCTTCCCAG	GACATGGAGA	ACTTCCTGAG	900
GGCCTGGAGT	CCCCCTGCAT	CATGGAGTCC	TTCTTAAGGA	CTGGAGCCTA	TGCAGGCACA	960
GAGTCCCTCA	GGACCAAGGA	GTCCCTCCTG	CAGGTGTGGA	GCCTTCC	GGATGCAGAG	1020
CCTTCCCAAG	ACATGGATT	CTTCCCAGGG	AGACAAAGCC	CTGTCAGGAG	CACAGCATCT	1080
TCAGGAGGAGA	GGTGGAGTCT	ATCTTGGGGA	AACCAAATT	CCAGATTTTC	CCAGAGGCTC	1140
AGCAACTCTG	GCCTCAGGCT	TCCTTCCCAG	AGGCAGCGTC	TGGGCTGTG	TGTGCTGTGG	1200
AGGAGGGATT	GCAGGATGGA	TGGAGCTGGG	ACTGGGGCTG	TCTGGGTGGC	TGGTATCCTC	1260
GTTTGATACA	GGTGGAGTCT	CTGTGCTCTC	ATAGAAG			1297

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: GenBank
(B) CLONE: 1216498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

Met Gly Arg Ala Met Val Val Arg Leu Gly Leu Gly Leu Leu Leu
5 10 15
Leu Ala Leu Leu Leu Pro Thr Gln Ile Tyr Cys Asn Gln Thr Ser
20 25 30
Val Ala Pro Phe Ser Gly Asn Gln Ser Ile Ser Ala Ala Pro Asn
35 40 45
Pro Thr Asn Ala Thr Thr Arg Ser Gly Cys Ser Ser Leu Gln Ser
50 55 60
Thr Ala Gly Leu Leu Ala Leu Ser Leu Ser Leu Leu His Leu Tyr
65 70 75
Cys

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: GenBank
(B) CLONE: 130989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile
5 10 15
Gly Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu
20 25 30
Cys Glu Lys His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg
35 40 45
Gly Arg Ala Val Cys Gly Gly Val Leu Val His Pro Gln Trp Val
50 55 60
Leu Thr Ala Ala His Cys Ile Arg Asn Lys Ser Val Ile Leu Leu
65 70 75
Gly Arg His Ser Leu Phe His Pro Glu Asp Thr Gly Gln Val Phe
80 85 90
Gln Val Ser His Ser Phe Pro His Pro Leu Tyr Asp Met Ser Leu
95 100 105
Leu Lys Asn Arg Phe Leu Arg Pro Gly Asp Asp Ser Ser His Asp
110 115 120
Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Glu Leu Thr Asp Ala
125 130 135
Val Lys Val Met Asp Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr
140 145 150
Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu Phe
155 160 165
Leu Thr Pro Lys Lys Leu Gln Cys Val Asp Leu His Val Ile Ser
170 175 180
Asn Asp Val Cys Ala Gln Val His Pro Gln Lys Val Thr Lys Phe
185 190 195

Met	Leu	Cys	Ala	Gly	Arg	Trp	Thr	Gly	Gly	Lys	Ser	Thr	Cys	Ser
200							205							210
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	Gly	Val	Leu	Gln	Gly
215								220						225
Ile	Thr	Ser	Trp	Gly	Ser	Glu	Pro	Cys	Ala	Leu	Pro	Glu	Arg	Pro
230								235						240
Ser	Leu	Tyr	Thr	Lys	Val	Val	His	Tyr	Arg	Lys	Trp	Ile	Lys	Asp
245								250						255
Thr	Ile	Val	Ala	Asn	Pro									
260														

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 2459993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

Met	Leu	Ala	Cys	Leu	Cys	Cys	Lys	Lys	Gly	Gly	Ile	Gly	Phe	Lys
5							10							15
Glu	Phe	Glu	Asn	Ala	Glu	Gly	Asp	Glu	Tyr	Val	Ala	Asp	Phe	Ser
20								25						30
Glu	Gln	Gly	Ser	Pro	Ala	Ala	Ala	Gln	Thr	Gly	Pro	Asp	Val	
35								40						45
Tyr	Val	Leu	Pro	Leu	Thr	Glu	Val	Ser	Leu	Pro	Met	Ala	Lys	Gln
50								55						60
Pro	Gly	Arg	Ser	Val	Gln	Leu	Leu	Lys	Ser	Thr	Asp	Leu	Gly	Arg
65								70						75
His	Ser	Leu	Leu	Tyr	Leu	Lys	Glu	Ile	Gly	His	Gly	Trp	Phe	Gly
80								85						90
Lys	Val	Phe	Leu	Gly	Glu	Val	His	Ser	Gly	Val	Ser	Gly	Thr	Gln
95								100						105
Val	Val	Val	Lys	Glu	Leu	Lys	Val	Ser	Ala	Ser	Val	Gln	Glu	Gln
110								115						120
Met	Gln	Phe	Leu	Glu	Glu	Ala	Gln	Pro	Tyr	Arg	Ala	Leu	Gln	His
125								130						135
Ser	Asn	Leu	Leu	Gln	Cys	Leu	Ala	Gln	Cys	Ala	Glu	Val	Thr	Pro
140								145						150
Tyr	Leu	Leu	Val	Met	Glu	Phe	Cys	Pro	Leu	Gly	Asp	Leu	Lys	Gly
155								160						165
Tyr	Leu	Arg	Ser	Cys	Arg	Val	Thr	Glu	Ser	Met	Ala	Pro	Asp	Pro
170								175						180
Leu	Thr	Leu	Gln	Arg	Met	Ala	Cys	Glu	Val	Ala	Cys	Gly	Val	Leu
185								190						195
His	Leu	His	Arg	His	Asn	Tyr	Val	His	Ser	Asp	Leu	Ala	Leu	Arg
200								205						210
Asn	Cys	Leu	Leu	Thr	Ala	Asp	Leu	Thr	Val	Lys	Val	Gly	Asp	Tyr
215								220						225
Gly	Leu	Ser	His	Cys	Lys	Tyr	Arg	Glu	Asp	Tyr	Leu	Val	Thr	Ala
230								235						240
Asp	Gln	Leu	Trp	Val	Pro	Leu	Arg	Trp	Ile	Ala	Pro	Glu	Leu	Val

Asp Glu Val His Gly Asn Leu Leu Val	245	Val Asp Gln Thr Lys Ser	255
260	265	270	
Ser Asn Val Trp Ser Leu Gly Val Thr Ile Trp Glu Leu Phe Glu	275	280	285
Leu Gly Ala Gln Pro Tyr Pro Gln His Ser Asp Arg Gln Val Leu	290	295	300
Ala Tyr Ala Val Arg Glu Gln Gln Leu Lys Leu Pro Lys Pro Gln	305	310	315
Leu Gln Leu Ala Leu Ser Asp Arg Trp Tyr Glu Val Met Gln Phe	320	325	330
Cys Trp Leu Gln Pro Glu Gln Arg Pro Thr Ala Glu Glu Val His	335	340	345
Leu Leu Leu Ser Tyr Leu Cys Ala Lys Gly Thr Thr Glu Leu Glu	350	355	360
Glu Glu Phe Glu Arg Arg Trp Arg Ser Leu Arg Pro Gly Gly Ser	365	370	375
Thr Gly Leu Gly Ser Gly Ser Ala Ala Pro Ala Ala Ala Thr Ala	380	385	390
Ala Ser Ala Glu Leu Thr Ala Ala Ser Ser Phe Pro Leu Leu Glu	395	400	405
Arg Phe Thr Ser Asp Gly Phe His Val Asp Ser Asp Asp Val Leu	410	415	420
Thr Val Thr Glu Thr Ser His Gly Leu Asn Phe Glu Tyr Lys Trp	425	430	435
Glu Ala Gly Cys Gly Ala Glu Glu Tyr Pro Pro Ser Gly Ala Ala	440	445	450
Ser Ser Pro Gly Ser Ala Ala Arg Leu Gln Glu Leu Cys Ala Pro	455	460	465
Asp Ser Ser Pro Pro Gly Val Val Pro Val Leu Ser Ala His Ser	470	475	480
Pro Ser Val Gly Ser Glu Tyr Phe Ile Arg Leu Glu Gly Ala Val	485	490	495
Pro Ala Ala Gly His Asp Pro Asp Cys Ala Gly Cys Ala Pro Ser	500	505	510
Pro Gln Ala Val Thr Asp Gln Asp Asn Asn Ser Glu Glu Ser Thr	515	520	525
Val Ala Ser Leu Ala Met Glu Pro Leu Leu Gly His Ala Pro Pro	530	535	540
Thr Glu Gly Leu Trp Gly Pro Cys Asp His His Ser His Arg Arg	545	550	555
Gln Gly Ser Pro Cys Pro Ser Arg Ser Pro Ser Pro Gly Thr Pro	560	565	570
Met Leu Pro Ala Glu Asp Ile Asp Trp Gly Val Ala Thr Phe Cys	575	580	585
Pro Pro Phe Phe Asp Asp Pro Leu Gly Ala Ser Pro Ser Gly Ser	590	595	600
Pro Gly Ala Gln Pro Ser Pro Ser Asp Glu Glu Pro Glu Glu Gly	605	610	615
Lys Val Gly Leu Ala Ala Gln Cys Gly His Trp Ser Ser Asn Met	620	625	630
Ser Ala Asn Asn Asn Ser Ala Ser Arg Asp Pro Glu Ser Trp Asp	635	640	645
Pro Gly Tyr Val Ser Ser Phe Thr Asp Ser Tyr Arg Asp Asp Cys	650	655	660
Ser Ser Leu Glu Gln Thr Pro Arg Ala Ser Pro Glu Val Gly His	665	670	675
Leu Leu Ser Gln Glu Asp Pro Arg Asp Phe Leu Pro Gly Leu Val	680	685	690
Ala Val Ser Pro Gly Gln Glu Pro Ser Arg Pro Phe Asn Leu Leu	695	700	705

Pro Leu Cys Pro Ala Lys Gly Leu Ala Pro Ala Ala Cys Leu Ile
 710 715 720
 Thr Ser Pro Trp Thr Glu Gly Ala Val Gly Gly Ala Glu Asn Pro
 725 730 735
 Ile Val Glu Pro Lys Leu Ala Gln Glu Ala Glu Gly Ser Ala Glu
 740 745 750
 Pro Gln Leu Pro Leu Pro Ser Val Pro Ser Pro Ser Cys Glu Gly
 755 760 765
 Ala Ser Leu Pro Ser Glu Glu Ala Ser Ala Pro Asp Ile Leu Pro
 770 775 780
 Ala Ser Pro Thr Pro Ala Ala Gly Ser Trp Val Thr Val Pro Glu
 785 790 795
 Pro Ala Pro Thr Leu Glu Ser Ser Gly Ser Ser Leu Gly Gln Glu
 800 805 810
 Ala Pro Ser Ser Glu Asp Glu Asp Thr Thr Glu Ala Thr Ser Gly
 815 820 825
 Val Phe Thr Asp Leu Ser Ser Asp Gly Pro His Thr Glu Lys Ser
 830 835 840
 Gly Ile Val Pro Ala Leu Arg Ser Leu Gln Lys Gln Val Gly Thr
 845 850 855
 Pro Asp Ser Leu Asp Ser Leu Asp Ile Pro Ser Ser Ala Ser Asp
 860 865 870
 Gly Gly Cys Glu Val Leu Ser Pro Ser Ala Ala Gly Pro Pro Gly
 875 880 885
 Gly Gln Pro Arg Ala Val Asp Ser Gly Tyr Asp Thr Glu Asn Tyr
 890 895 900
 Glu Ser Pro Glu Phe Val Leu Lys Glu Ala His Glu Ser Ser Glu
 905 910 915
 Pro Glu Ala Phe Gly Glu Pro Ala Ser Glu Gly Glu Ser Pro Gly
 920 925 930
 Pro Asp Pro Leu Leu Ser Val Ser Leu Gly Gly Leu Ser Lys Lys
 935 940 945
 Ser Pro Tyr Arg Asp Ser Ala Tyr Phe Ser Asp Leu Asp Ala Glu
 950 955 960
 Ser Glu Pro Thr Phe Gly Pro Glu Lys His Ser Gly Ile Gln Asp
 965 970 975
 Ser Gln Lys Glu Gln Asp Leu Arg Ser Pro Pro Ser Pro Gly His
 980 985 990
 Gln Ser Val Gln Ala Phe Pro Arg Ser Ala Val Ser Ser Glu Val
 995 1000 1005
 Leu Ser Pro Pro Gln Gln Ser Glu Glu Pro Leu Pro Glu Val Pro
 1010 1015 1020
 Arg Pro Glu Pro Leu Gly Ala Gln Gly Pro Val Gly Val Gln Pro
 1025 1030 1035
 Val Pro Gly Pro Ser His Ser Lys Cys Phe Pro Leu Thr Ser Val
 1040 1045 1050
 Pro Leu Ile Ser Glu Gly Ser Gly Thr Glu Pro Gln Gly Pro Ser
 1055 1060 1065
 Gly Gln Leu Ser Gly Arg Ala Gln Gln Gly Gln Met Gly Asn Pro
 1070 1075 1080
 Ser Thr Pro Arg Ser Pro Leu Cys Leu Ala Leu Pro Gly His Pro
 1085 1090 1095
 Gly Ala Leu Glu Gly Arg Pro Glu Glu Asp Glu Asp Thr Glu Asp
 1100 1105 1110
 Ser Glu Glu Ser Asp Glu Glu Leu Arg Cys Tyr Ser Val Gln Glu
 1115 1120 1125
 Pro Ser Glu Asp Ser Glu Glu Pro Pro Ala Val Pro Val Val
 1130 1135 1140
 Val Ala Glu Ser Gln Ser Ala Arg Asn Leu Arg Ser Leu Leu Lys
 1145 1150 1155
 Met Pro Ser Leu Leu Ser Glu Ala Phe Cys Asp Asp Leu Glu Arg

1160	1165	1170
Lys Lys Lys Ala Val Ser Phe Phe Asp Asp Val Thr Val Tyr Leu		
1175	1180	1185
Phe Asp Gln Glu Ser Pro Thr Arg Glu Thr Gly Glu Pro Phe Pro		
1190	1195	1200
Ser Thr Lys Glu Ser Leu Pro Thr Phe Leu Glu Gly Gly Pro Ser		
1205	1210	1215
Ser Pro Ser Ala Thr Gly Leu Pro Leu Arg Ala Gly His Ser Pro		
1220	1225	1230
Asp Ser Ser Ala Pro Glu Pro Gly Ser Arg Phe Glu Trp Asp Gly		
1235	1240	1245
Asp Phe Pro Leu Val Pro Gly Lys Ala Ala Leu Val Thr Glu Leu		
1250	1255	1260
Asp Pro Ala Asp Pro Val Leu Ala Ala Pro Pro Thr Pro Ala Ala		
1265	1270	1275
Pro Phe Ser Arg Phe Thr Val Ser Pro Thr Pro Ala Ser Arg Phe		
1280	1285	1290
Ser Ile Thr His Ile Ser Asp Ser Asp Ala Gln Ser Val Gly Gly		
1295	1300	1305
Pro Ala Ala Gly Ala Gly Gly Arg Tyr Thr Glu Ala		
1310	1315	